



SEQUENCE LISTING

<110> FULTON, CHANDLER
LAI, ELAINE Y.

<120> THIAMINASES AND THIAMINASE GENES FOR USE IN APOPTOTIC THERAPIES

<130> 073442-0301

<140> 09/675,509
<141> 2000-09-29

<150> 60/052,377
<151> 1997-07-11

<150> 60/087,526
<151> 1998-06-01

<150> 60/156,952
<151> 1999-09-29

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 3078

<212> DNA

<213> Naegleria gruberi

<400> 1

atgtccactc aaccaaagac actcactgtt ggtctttcc catatcttcc ttcttggaaat 60
gaaaatggca acgaagttaa attgatcaat ttgatcaagg atgtttgcc aactcaggtt 120
tccggatata atatcgata taccgaattt gattgttaca gtgatgtctag tcttcaaagt 180
cttccagatg ttttctcaac tgatagcatt ttccttccat atcttgtttc tttgggtgggt 240
gtcaagagtt tggatgaatc attgggtcgt ggtgttactg gtgatttgca tagttttgtt 300
tcctcaagtg cctctgtcaa tggttccgtt tatggttcc cacaatactt gtgctcaaac 360
tttttattgt cctcaccaaa tggtaactcaa caagcatctt cccttttaga attggctcaa 420
aagggttgggtt atgaacaaat tggttatcca gatgttgcct cttctagttc tttcacagtt 480
ttcggattgt atcaacaatt actccaatca tcatcatcag ctgcagttga tatcaaggcc 540
tctgatctc cacaatctgg tgaccaagtc aacaaggata tcactcaaaa atatagaacc 600
attttggatt caacagttgt tgcctctcaa agagaatata ttaactctgt aaagcaaggt 660
aaaccaattt caaactacta tgcggatat agtcaaagta tggtaaaat taaggatatac 720
atcagagatc aacaatacaa tggtaactc attggtagct ctgataagcc atacgtttat 780
actgatgttt tggctttgaa ttccaatttg tggatgaaa agcaaaaagggt tgctgttgaa 840
gttatcaaga atttattgac taatacttta gttttggact tggatgggtct cggattaaact 900
ctcccagcca acaagaatgg tattgctcat ttggctaaat catcaaactt ttatgctcaa 960
ttgagccaaac aattcgatgc caaggaaaagt gaagtttagag ttttgagatg tggatggctt 1020
gctaacaagg aagttaaagaa ttgtgctggc gtcttgagac cattccttca acatattgt 1080
gttgctactt tgcgttgcatt gactgctgac actgtcgaaa aggctaagag tggtcaccc 1140
ggtatgccaa ttggatgtc accaattgcc tatgtttgt ggaagttctt cttcaaacta 1200
tctaaggatg atgtcaattt gttgaacaga gatagattt ttttgagatg tggatggctt 1260
tgtacattgc ttatgccat gttgcaccc actgattgtt actgtgatgtt ggtatgtctc 1320
aagaatttca gaagtttgca ttccaagact cctggtcacc cagaatatgg tcacactgaa 1380
ggtgttgcatt ctactactgg tccattgggtt caaggatgtt gtaatgtat tggatggctt 1440
ctctctgaag ctcaacttggc tgctcggtt aataaggatg gacaatataat ctttgatc 1500
cacacctatg tttccttgg tggatggatgtt ttgatggac gttgtctc 1560

tcatttgctg gtcaccaaaa gttgaacaag ttgattgtt tctatgatga caatagtatt 1620
 actattgatg gtaagactga attgacctt actcaaaata ctccagaagt catgagaggt 1680
 tttggatggc acgttaattgt tgtcgacaag gctgataatg acttgggttgg tattaaggaa 1740
 gctattttgg aagtcacac tgttactgac aagccaatca tgatcggtt taagactaca 1800
 attggttatt cctcaaagggt tcaaggtaact gctaagggttc acggttctcc attgggtgct 1860
 gatggattga agaatttggaa gcaaacttgt gggttcaactg gtaatgattt cttccatgtt 1920
 ccagaaatttgc tcaagaaaggaa ctttgcact gtcattaata gaaatagtga aaagctct 1980
 caatggaaagc aagttaaatc tgcctatgtat accactcatg ctactgaatc ccaactcctc 2040
 caaagaatga ttaatcacga attggaaaggat gatgttatgg aaaagttgcc aaaatacctc 2100
 gaacaaaaga agattgctac cagatctaca tctcaacaag tttgaatgc catctatcca 2160
 ctcattcctt ctctcggttgg tggttcagct gacttgactc catccaactt gactgatgt 2220
 actggatgtc aagatttcca accaaacaat agagttggta gatatatcag atttgggtc 2280
 cgtgaacatg ccatgggtgc tattgccaat ggtattctct atcatgggt tcttagaacc 2340
 tatgttggtt cattcttgc ctttgcctca tatgctttgg gtgctatcag attgagtgc 2400
 ttgtctggtc ttccaaatat ttatgtttc actcatgaca gtattggct tggtaagat 2460
 ggtccaaactc accaacctgt tgaagttta ccaatgttga tagccattcc aaatcacatt 2520
 gtttcagac ctgctgatgg tagagaaacc agtggtgctt atttggggc tggtaatca 2580
 aagaagactc catcctcaat gattcttct cgtcaagatt tgccacaatt gactggtaact 2640
 gatatttcaa aggttgc ctttgcctat gttatccaag gtgatgctac tcctgatgtt 2700
 gtccttggc gtactgggtc tgaagttcc ctcatgggtt aagctgctga aaagttgaag 2760
 gctaacccttta aggttaacgt tggccatg ccaagttggg aattgtttgt tggtaatca 2820
 gaagaataca ggaagactgt cttccagat ggtattccag ttgtcagtgcc gaaagcttca 2880
 tcaacctttg gttggacaag ctttgcac tatgctgtt gtatgactac ttccgggtc 2940
 agtgctgctg ctgaagaagt ttacaaactc ctcagattt cctcagacaa tggtaatca 3000
 aaggccacca aattgggttac caagtatggt aagcaagctc caagactcag cttgtcttt 3060
 gttggtaag aactctaa 3078

<210> 2
 <211> 1025
 <212> PRT
 <213> Naegleria gruberi

<400> 2
 Met Ser Thr Gln Pro Lys Thr Leu Thr Val Gly Leu Phe Pro Tyr Leu
 1 5 10 15

Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile
 20 25 30

Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
 35 40 45

Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
 50 55 60

Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
 65 70 75 80

Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
 85 90 95

His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
 100 105 110

Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly
 115 120 125

Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr
130 135 140

Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Ser Phe Thr Val
145 150 155 160

Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ser Ala Ala Val
165 170 175

Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
180 185 190

Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala
195 200 205

Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser
210 215 220

Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile
225 230 235 240

Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys
245 250 255

Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp
260 265 270

Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn
275 280 285

Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn
290 295 300

Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln
305 310 315 320

Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg
325 330 335

Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu
340 345 350

Arg Pro Phe Leu Gln His Ile Ala Val Ala Thr Leu Arg Cys Leu Thr
355 360 365

Ala Asp Thr Val Glu Lys Ala Lys Ser Gly His Pro Gly Met Pro Ile
370 375 380

Gly Met Ser Pro Ile Ala Tyr Val Leu Trp Lys Phe Phe Phe Lys Ser
385 390 395 400

Ser Lys Asp Asp Val Asn Trp Leu Asn Arg Asp Arg Phe Val Leu Ser
405 410 415

Asn Gly His Gly Cys Thr Leu Leu Tyr Ala Met Leu His Leu Thr Asp
420 425 430

Cys Asn Leu Ser Leu Asp Asp Leu Lys Asn Phe Arg Ser Leu His Ser
 435 440 445
 Lys Thr Pro Gly His Pro Glu Tyr Gly His Thr Glu Gly Val Asp Ala
 450 455 460
 Thr Thr Gly Pro Leu Gly Gln Gly Val Cys Asn Ala Ile Gly Met Ala
 465 470 475 480
 Leu Ser Glu Ala His Leu Ala Ala Arg Phe Asn Lys Asp Gly Gln Asn
 485 490 495
 Ile Phe Asp His His Thr Tyr Val Phe Leu Gly Asp Gly Cys Leu Met
 500 505 510
 Glu Arg Val Ala Met Glu Gly Leu Ser Phe Ala Gly His Gln Lys Leu
 515 520 525
 Asn Lys Leu Ile Val Phe Tyr Asp Asp Asn Ser Ile Thr Ile Asp Gly
 530 535 540
 Lys Thr Glu Leu Thr Phe Thr Gln Asn Thr Pro Glu Val Met Arg Gly
 545 550 555 560
 Phe Gly Trp His Val Ile Val Val Asp Lys Ala Asp Asn Asp Leu Val
 565 570 575
 Gly Ile Lys Glu Ala Ile Leu Glu Ala His Thr Val Thr Asp Lys Pro
 580 585 590
 Ile Met Ile Val Cys Lys Thr Thr Ile Gly Tyr Ser Ser Lys Val Gln
 595 600 605
 Gly Thr Ala Lys Val His Gly Ser Pro Leu Gly Ala Asp Gly Leu Lys
 610 615 620
 Asn Leu Lys Glu Thr Cys Gly Phe Thr Gly Asn Asp Phe Phe His Val
 625 630 635 640
 Pro Glu Ile Val Arg Lys Asp Phe Ala Thr Val Ile Asn Arg Asn Ser
 645 650 655
 Glu Lys Leu Ser Gln Trp Lys Gln Val Lys Ser Ala Tyr Asp Thr Thr
 660 665 670
 His Ala Thr Glu Ser Gln Leu Leu Gln Arg Met Ile Asn His Glu Leu
 675 680 685
 Glu Gly Asp Val Met Glu Lys Leu Pro Lys Tyr Leu Glu Gln Lys Lys
 690 695 700
 Ile Ala Thr Arg Ser Thr Ser Gln Gln Val Leu Asn Ala Ile Tyr Pro
 705 710 715 720
 Leu Ile Pro Ser Leu Val Gly Gly Ser Ala Asp Leu Thr Pro Ser Asn
 725 730 735

Leu Thr Asp Val Thr Gly Cys Gln Asp Phe Gln Pro Asn Asn Arg Val
740 745 750

Gly Arg Tyr Ile Arg Phe Gly Val Arg Glu His Ala Met Val Ala Ile
755 760 765

Ala Asn Gly Ile Leu Tyr His Gly Val Leu Arg Thr Tyr Val Gly Thr
770 775 780

Phe Leu Asn Phe Ala Ser Tyr Ala Leu Gly Ala Ile Arg Leu Ser Ala
785 790 795 800

Leu Ser Gly Leu Pro Asn Ile Tyr Val Phe Thr His Asp Ser Ile Gly
805 810 815

Leu Gly Gln Asp Gly Pro Thr His Gln Pro Val Glu Val Leu Pro Met
820 825 830

Leu Ile Ala Ile Pro Asn His Ile Val Phe Arg Pro Ala Asp Gly Arg
835 840 845

Glu Thr Ser Gly Ala Tyr Leu Trp Ala Val Gln Ser Lys Lys Thr Pro
850 855 860

Ser Ser Met Ile Leu Ser Arg Gln Asp Leu Pro Gln Leu Thr Gly Thr
865 870 875 880

Asp Ile Ser Lys Val Ala Leu Gly Ala Tyr Val Ile Gln Gly Asp Ala
885 890 895

Thr Pro Asp Val Val Leu Val Gly Thr Gly Ser Glu Val Ser Leu Met
900 905 910

Val Glu Ala Ala Glu Lys Leu Lys Ala Asn Leu Lys Val Asn Val Val
915 920 925

Ser Met Pro Ser Trp Glu Leu Phe Val Arg Gln Ser Glu Glu Tyr Arg
930 935 940

Lys Thr Val Phe Pro Asp Gly Ile Pro Val Val Ser Ala Glu Ala Ser
945 950 955 960

Ser Thr Phe Gly Trp Thr Ser Phe Ala His Tyr Ala Val Gly Met Thr
965 970 975

Thr Phe Gly Ala Ser Ala Ala Glu Glu Val Tyr Lys Leu Leu Lys
980 985 990

Ile Thr Ser Asp Asn Val Ala Glu Lys Ala Thr Lys Leu Val Thr Lys
995 1000 1005

Tyr Gly Lys Gln Ala Pro Arg Leu Ser Leu Ser Leu Val Gly Glu Glu
1010 1015 1020

Leu
1025

<210> 3
 <211> 1068
 <212> DNA
 <213> Naegleria gruberi

 <220>
 <221> CDS
 <222> (1)..(1068)

 <400> 3
 atg tcc actcaa cca aag aca ctc act gtt ggt ctc ttc cca tat ctt 48
 Met Ser Thr Gln Pro Lys Thr Leu Thr Val Gly Leu Phe Pro Tyr Leu
 1 5 10 15

 cct tct tgg aat gaa aat ggc aac gaa gtt aaa ttg atc aat ttg atc 96
 Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile
 20 25 30

 aag gat gtt ttg cca act cag gtt tcc gga tat aat atc gaa tat acc 144
 Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
 35 40 45

 gaa ttt gat tgt tac agt gat gct agt ctt caa agt ctt cca gat gtt 192
 Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
 50 55 60

 ttc tca act gat agc att ttc ctt cca tat ctt gtt tct ttg ggt ggt 240
 Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
 65 70 75 80

 gtc aag agt ttg gat gaa tca ttg gtt cgt ggt gtt act ggt gat ttg 288
 Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
 85 90 95

 cat agt ttt gtt tcc tca agt gcc tct gtc aat ggt tcc gtt tat ggt 336
 His Ser Phe Val Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
 100 105 110

 ttc cca caa tac ttg tgc tca aac ttt tta ttg tcc tca cca aat ggt 384
 Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly
 115 120 125

 act caa caa gca tct tcc ctt tta gaa ttg gct caa aag gtt ggt tat 432
 Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr
 130 135 140

 gaa caa att gtt tat cca gat gtt gcc tct tct agt tct ttc aca gtt 480
 Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Phe Thr Val
 145 150 155 160

 ttc gga ttg tat caa caa tta ctc caa tca tca tca tca gct gca gtt 528
 Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ser Ala Ala Val
 165 170 175

 gat atc aag gcc tct gat ctt cca caa tct ggt gac caa gtc aac aag 576
 Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
 180 185 190

gat atc actcaa aaa tat aga acc att ttg gat tca aca gtt gtt gcc		624
Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala		
195 200 205		
tct caa aga gaa tat att aac tct gta aag caa ggt aaa cca att tca		672
Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser		
210 215 220		
aac tac tat gtc gga tat agt gaa agt atg tgt gaa att aag gat atc		720
Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile		
225 230 235 240		
atc aga gat caa caa tac aat gtt caa ctc att ggt acc tct gat aag		768
Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys		
245 250 255		
cca tac gtt tat act gat gtt ttg gct ttg aat tcc aat ttg tgt gat		816
Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp		
260 265 270		
gaa aag caa aag gtt gct gtt gaa gtt atc aag aat tta ttg act aat		864
Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn		
275 280 285		
act tta gtt ttg gac ttg ggt ctc gga tta act ctc cca gcc aac		912
Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn		
290 295 300		
aag aat ggt att gct cat ttg gct aaa tca tca aac ttt tat gct caa		960
Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln		
305 310 315 320		
ttg agc caa caa ttc gat gcc aag gaa agt gaa gtt aga gtt ttg aga		1008
Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg		
325 330 335		
tgt gtt gac ttt gct aac aag gaa gtt aag aat tgt gct ggt gtc ttg		1056
Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu		
340 345 350		
aga cca ttc ctt		1068
Arg Pro Phe Leu		
355		
<210> 4		
<211> 356		
<212> PRT		
<213> Naegleria gruberi		
<400> 4		
Met Ser Thr Gln Pro Lys Thr Leu Thr Val Gly Leu Phe Pro Tyr Leu		
1 5 10 15		
Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile		
20 25 30		

Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
 35 40 45

Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
 50 55 60

Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
 65 70 75 80

Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
 85 90 95

His Ser Phe Val Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
 100 105 110

Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly
 115 120 125

Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr
 130 135 140

Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Phe Thr Val
 145 150 155 160

Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ala Ala Val
 165 170 175

Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
 180 185 190

Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala
 195 200 205

Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser
 210 215 220

Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile
 225 230 235 240

Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys
 245 250 255

Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp
 260 265 270

Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn
 275 280 285

Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn
 290 295 300

Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln
 305 310 315 320

Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg
 325 330 335

Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu
 340 345 350

Arg Pro Phe Leu
 355

<210> 5
 <211> 412
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 5
 Ala Asp Asp Val Lys Gln Leu Lys Ser Lys Phe Gly Phe Asn Pro Asp
 1 5 10 15

Lys Ser Phe Val Val Pro Gln Glu Val Tyr Asp His Tyr Gln Lys Thr
 20 25 30

Ile Leu Lys Pro Gly Val Glu Ala Asn Asn Lys Trp Asn Lys Leu Phe
 35 40 45

Ser Glu Tyr Gln Lys Lys Phe Pro Glu Leu Gly Ala Glu Leu Ala Arg
 50 55 60

Arg Leu Ser Gly Gln Leu Pro Ala Asn Trp Glu Ser Lys Leu Pro Thr
 65 70 75 80

Tyr Thr Ala Lys Asp Ser Ala Val Ala Thr Arg Lys Leu Ser Glu Thr
 85 90 95

Val Leu Glu Asp Val Tyr Asn Gln Leu Pro Glu Leu Ile Gly Gly Ser
 100 105 110

Ala Asp Leu Thr Pro Ser Asn Leu Thr Arg Trp Lys Glu Ala Leu Asp
 115 120 125

Phe Gln Pro Pro Ser Ser Gly Ser Gly Asn Tyr Ser Gly Arg Tyr Ile
 130 135 140

Arg Tyr Gly Ile Arg Glu His Ala Met Gly Ala Ile Met Asn Gly Ile
 145 150 155 160

Ser Ala Phe Gly Ala Asn Tyr Lys Pro Tyr Gly Gly Thr Phe Leu Asn
 165 170 175

Phe Val Ser Tyr Ala Ala Gly Ala Val Arg Leu Ser Ala Leu Ser Gly
 180 185 190

His Pro Val Ile Trp Val Ala Thr His Asp Ser Ile Gly Val Gly Glu
 195 200 205

Asp Gly Pro Thr His Gln Pro Ile Glu Thr Leu Ala His Phe Arg Ser
 210 215 220

Leu Pro Asn Ile Gln Val Trp Arg Pro Ala Asp Gly Asn Glu Val Ser
 225 230 235 240

Ala Ala Tyr Lys Asn Ser Leu Glu Ser Lys His Thr Pro Ser Ile Ile
 245 250 255
 Ala Leu Ser Arg Gln Asn Leu Pro Gln Leu Glu Gly Ser Ser Ile Glu
 260 265 270
 Ser Ala Ser Lys Gly Gly Tyr Val Leu Gln Asp Val Ala Asn Pro Asp
 275 280 285
 Ile Ile Leu Val Ala Thr Gly Ser Glu Val Ser Leu Ser Val Glu Ala
 290 295 300
 Ala Lys Thr Leu Ala Ala Lys Asn Ile Lys Ala Arg Val Val Ser Leu
 305 310 315 320
 Pro Asp Phe Phe Thr Phe Asp Lys Gln Pro Leu Glu Tyr Arg Leu Ser
 325 330 335
 Val Leu Pro Asp Asn Val Pro Ile Met Ser Val Glu Val Leu Ala Thr
 340 345 350
 Thr Cys Trp Gly Lys Tyr Ala His Gln Ser Phe Gly Ile Asp Arg Phe
 355 360 365
 Gly Ala Ser Gly Lys Ala Pro Glu Val Phe Lys Phe Phe Gly Phe Thr
 370 375 380
 Pro Glu Gly Val Ala Glu Arg Ala Gln Lys Thr Ile Ala Phe Tyr Lys
 385 390 395 400
 Gly Asp Lys Leu Ile Ser Pro Leu Lys Lys Ala Phe
 405 410

<210> 6
 <211> 398
 <212> PRT
 <213> Craterostigma plantagineum

<400> 6
 Pro Lys Glu Ala Glu Ala Thr Arg Lys Asn Leu Gly Trp Pro Tyr Glu
 1 5 10 15
 Pro Phe His Val Pro Asp Asp Val Lys Lys His Trp Ser Arg His Ile
 20 25 30
 Ala Glu Gly Ala Ala Leu Glu Ser Ala Trp Asn Ala Lys Phe Ala Glu
 35 40 45
 Phe Gln Lys Lys Phe Pro Glu Glu Ala Ala Asp Leu Lys Ser Ile Ile
 50 55 60
 Thr Gly Glu Leu Pro Thr Asn Trp Glu Ser Ile Phe Pro Thr Tyr Thr
 65 70 75 80
 Pro Glu Asn Pro Gly Leu Pro Thr Arg Thr Leu Ser His Gln Ile Leu
 85 90 95

Asn Gly Leu Gly Asp Val Leu Pro Gly Leu Leu Gly Gly Ser Ala Asp
 100 105 110
 Leu Thr Leu Ser Asn Met Ala Phe Leu Lys Asn Ser Gly Asp Phe Gln
 115 120 125
 Lys Lys Ser Pro Gly Glu Arg Asn Val Lys Phe Gly Ala Arg Glu His
 130 135 140
 Ala Met Gly Ser Ile Cys Asn Gly Leu Ala Leu His Ser Pro Gly Leu
 145 150 155 160
 Leu Pro Tyr Cys Ala Thr Tyr Phe Val Phe Thr Asp Tyr Met Arg Ala
 165 170 175
 Ala Met Arg Ile Ser Ala Leu Ser Lys Ala Arg Val Leu Tyr Ile Met
 180 185 190
 Thr His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro
 195 200 205
 Val Glu His Leu Ala Ser Phe Arg Ala Met Pro Asn Ile Leu Thr Leu
 210 215 220
 Arg Pro Ala Asp Gly Asn Glu Thr Ala Gly Ala Tyr Arg Ala Ala Val
 225 230 235 240
 Gln Asn Gly Glu Arg Pro Ser Ile Leu Val Leu Ala Arg Gln Lys Leu
 245 250 255
 Pro Gln Leu Pro Gly Thr Ser Ile Glu Gly Val Ser Lys Gly Gly Tyr
 260 265 270
 Val Ile Ser Asp Asn Ser Arg Gly Gly Asn Ser Lys Pro Asp Val Ile
 275 280 285
 Leu Ile Gly Thr Gly Ser Glu Leu Glu Ile Ala Ala Arg Ala Gly Asp
 290 295 300
 Glu Leu Arg Lys Glu Gly Lys Lys Val Arg Val Val Ser Leu Val Cys
 305 310 315 320
 Trp Glu Leu Phe Ala Glu Gln Ser Glu Lys Tyr Arg Glu Thr Val Leu
 325 330 335
 Pro Ser Gly Val Thr Ala Arg Val Ser Val Glu Ala Gly Ser Thr Phe
 340 345 350
 Gly Trp Glu Arg Phe Ile Gly Pro Lys Gly Lys Ala Val Gly Ile Asp
 355 360 365
 Arg Phe Gly Ala Ser Ala Pro Ala Glu Arg Leu Phe Lys Glu Phe Gly
 370 375 380
 Ile Thr Val Glu Ala Val Val Ala Ala Lys Glu Ile Cys
 385 390 395

<210> 7
 <211> 402
 <212> PRT
 <213> Escherichia coli

<400> 7
 Glu Glu Glu Val Ala Leu Ala Arg Gln Lys Leu Gly Trp His His Pro
 1 5 10 15

Pro Phe Glu Ile Pro Lys Glu Ile Tyr His Ala Trp Asp Ala Arg Glu
 20 25 30

Lys Gly Glu Lys Ala Gln Gln Ser Trp Asn Glu Lys Phe Ala Ala Tyr
 35 40 45

Lys Lys Ala His Pro Gln Leu Ala Glu Glu Phe Thr Arg Arg Met Ser
 50 55 60

Gly Gly Leu Pro Lys Asp Trp Glu Lys Thr Thr Gln Lys Tyr Ile Asn
 65 70 75 80

Glu Leu Gln Ala Asn Pro Ala Lys Ile Ala Thr Arg Lys Ala Ser Gln
 85 90 95

Asn Thr Leu Asn Ala Tyr Gly Pro Met Leu Pro Glu Leu Leu Gly Gly
 100 105 110

Ser Ala Asp Leu Ala Pro Ser Asn Leu Thr Ile Trp Lys Gly Ser Val
 115 120 125

Ser Leu Lys Glu Asp Pro Ala Gly Asn Tyr Ile His Tyr Gly Val Arg
 130 135 140

Glu Phe Gly Met Thr Ala Ile Ala Asn Gly Ile Ala His His Gly Gly
 145 150 155 160

Phe Val Pro Tyr Thr Ala Thr Phe Leu Met Phe Val Glu Tyr Ala Arg
 165 170 175

Asn Ala Ala Arg Met Ala Ala Leu Met Lys Ala Arg Gln Ile Met Val
 180 185 190

Tyr Thr His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln
 195 200 205

Ala Val Glu Gln Leu Ala Ser Leu Arg Leu Thr Pro Asn Phe Ser Thr
 210 215 220

Trp Arg Pro Cys Asp Gln Val Glu Ala Ala Val Gly Trp Lys Leu Ala
 225 230 235 240

Val Glu Arg His Asn Gly Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn
 245 250 255

Leu Ala Gln Val Glu Arg Thr Pro Asp Gln Val Lys Glu Ile Ala Arg
 260 265 270

Gly Gly Tyr Val Leu Lys Asp Ser Gly Gly Lys Pro Asp Ile Ile Leu
 275 280 285

Ile Ala Thr Gly Ser Glu Met Glu Ile Thr Leu Gln Ala Ala Glu Lys
 290 295 300

Leu Ala Gly Glu Gly Arg Asn Val Arg Val Val Ser Leu Pro Ser Thr
 305 310 315 320

Asp Ile Phe Asp Ala Gln Asp Glu Glu Tyr Arg Glu Ser Val Leu Pro
 325 330 335

Ser Asn Val Ala Ala Arg Val Ala Val Glu Ala Gly Ile Ala Asp Tyr
 340 345 350

Trp Tyr Lys Tyr Val Gly Leu Lys Gly Ala Ile Val Gly Met Thr Gly
 355 360 365

Tyr Gly Glu Ser Ala Pro Ala Asp Lys Leu Phe Pro Phe Phe Gly Phe
 370 375 380

Thr Ala Glu Asn Ile Val Ala Lys Ala His Lys Val Leu Gly Val Lys
 385 390 395 400

Gly Ala

<210> 8

<211> 400

<212> PRT

<213> Bacillus subtilis

<400> 8

Lys Glu Glu Ser Lys Leu Thr Lys Glu Ala Tyr Ala Trp Thr Tyr Glu
 1 5 10 15

Glu Asp Phe Tyr Val Pro Ser Glu Val Tyr Glu His Phe Ala Val Ala
 20 25 30

Val Lys Glu Ser Gly Glu Lys Lys Glu Gln Glu Trp Asn Ala Gln Phe
 35 40 45

Ala Lys Tyr Lys Glu Val Tyr Pro Glu Leu Ala Glu Gln Leu Glu Leu
 50 55 60

Ala Ile Lys Gly Glu Leu Pro Lys Asp Trp Asp Gln Glu Val Pro Val
 65 70 75 80

Tyr Glu Lys Gly Ser Ser Leu Ala Ser Arg Ala Ser Ser Gly Glu Val
 85 90 95

Leu Asn Gly Leu Ala Lys Lys Ile Pro Phe Phe Val Gly Gly Ser Ala
 100 105 110

Asp Leu Ala Gly Ser Asn Lys Thr Thr Ile Lys Asn Ala Gly Asp Phe
 115 120 125

Thr Ala Val Asp Tyr Ser Gly Lys Asn Phe Trp Phe Gly Val Arg Glu
 130 135 140

Phe Ala Met Gly Ala Ala Leu Asn Gly Met Ala Leu His Gly Gly Leu
 145 150 155 160

Arg Val Phe Gly Gly Thr Phe Phe Val Phe Ser Asp Tyr Leu Arg Pro
 165 170 175

Ala Ile Arg Leu Ala Ala Leu Met Gly Leu Pro Val Thr Tyr Val Phe
 180 185 190

Thr His Asp Ser Ile Ala Val Gly Glu Asp Gly Pro Thr His Glu Pro
 195 200 205

Val Glu Gln Leu Ala Ser Leu Arg Ala Met Pro Asn Leu Ser Leu Ile
 210 215 220

Arg Pro Ala Asp Gly Asn Glu Thr Ala Ala Ala Trp Lys Leu Ala Val
 225 230 235 240

Gln Ser Thr Asp His Pro Thr Ala Leu Val Leu Thr Arg Gln Asn Leu
 245 250 255

Pro Thr Ile Asp Gln Thr Ser Glu Glu Ala Leu Ala Gly Val Glu Lys
 260 265 270

Gly Ala Tyr Val Val Ser Lys Ser Lys Asn Glu Thr Pro Asp Ala Leu
 275 280 285

Leu Ile Ala Ser Gly Ser Glu Val Gly Leu Ala Ile Glu Ala Gln Ala
 290 295 300

Glu Leu Ala Lys Glu Asn Ile Asp Val Ser Val Val Ser Met Pro Ser
 305 310 315 320

Met Asp Arg Phe Glu Lys Gln Ser Asp Glu Tyr Lys Asn Glu Val Leu
 325 330 335

Pro Ala Asp Val Lys Lys Arg Leu Ala Ile Glu Met Gly Ser Ser Phe
 340 345 350

Gly Trp Gly Lys Tyr Thr Gly Leu Glu Gly Asp Val Leu Gly Ile Asp
 355 360 365

Arg Phe Gly Ala Ser Ala Pro Gly Glu Thr Ile Ile Asn Glu Tyr Gly
 370 375 380

Phe Ser Val Pro Asn Val Val Asn Arg Val Lys Ala Leu Ile Asn Lys
 385 390 395 400

<210> 9
 <211> 391
 <212> PRT
 <213> Mycoplasma genitalium

<400> 9
 Glu Val Asp Phe Gln Leu Phe Glu Lys Arg Thr Asn Thr Asn Phe Asn
 1 5 10 15
 Phe Phe Asn Tyr Pro Asp Ser Ile Tyr His Trp Phe Lys Gln Thr Val
 20 25 30
 Ile Glu Arg Gln Lys Gln Ile Lys Glu Asp Tyr Asn Asn Leu Leu Ile
 35 40 45
 Ser Leu Lys Asp Lys Pro Leu Phe Lys Lys Phe Thr Asn Trp Ile Asp
 50 55 60
 Ser Asp Phe Gln Ala Leu Tyr Leu Asn Gln Leu Asp Glu Lys Lys Val
 65 70 75 80
 Ala Lys Lys Asp Ser Ala Thr Arg Asn Tyr Leu Lys Asp Phe Leu Asn
 85 90 95
 Gln Ile Asn Asn Pro Asn Ser Asn Leu Tyr Cys Leu Asn Ala Asp Val
 100 105 110
 Ser Arg Ser Cys Phe Ile Lys Ile Gly Asp Asp Asn Leu His Glu Asn
 115 120 125
 Pro Cys Ser Arg Asn Ile Gln Ile Gly Ile Arg Glu Phe Ala Met Ala
 130 135 140
 Thr Ile Met Asn Gly Met Ala Leu His Gly Gly Ile Lys Val Met Gly
 145 150 155 160
 Gly Thr Phe Leu Ala Phe Ala Asp Tyr Ser Lys Pro Ala Ile Arg Leu
 165 170 175
 Gly Ala Leu Met Asn Leu Pro Val Phe Tyr Val Tyr Thr His Asp Ser
 180 185 190
 Tyr Gln Val Gly Gly Asp Gly Pro Thr His Gln Pro Tyr Asp Gln Leu
 195 200 205
 Pro Met Leu Arg Ala Ile Glu Asn Val Cys Val Phe Arg Pro Cys Asp
 210 215 220
 Glu Lys Glu Thr Cys Ala Gly Phe Asn Tyr Gly Leu Leu Ser Gln Asp
 225 230 235 240
 Gln Thr Thr Val Leu Val Leu Thr Arg Gln Pro Leu Lys Ser Ile Asp
 245 250 255
 Asn Thr Asp Ser Leu Lys Thr Leu Lys Gly Gly Tyr Ile Leu Leu Asp
 260 265 270
 Arg Lys Gln Pro Asp Leu Ile Ile Ala Ala Ser Gly Ser Glu Val Gln
 275 280 285
 Leu Ala Ile Glu Phe Glu Lys Val Leu Thr Lys Gln Asn Val Lys Val
 290 295 300

Arg Ile Leu Ser Val Pro Asn Ile Thr Leu Leu Leu Lys Gln Asp Glu
 305 310 315 320

Lys Tyr Leu Lys Ser Leu Phe Asp Ala Asn Ser Ser Leu Ile Thr Ile
 325 330 335

Glu Ala Ser Ser Ser Tyr Glu Trp Phe Cys Phe Lys Lys Tyr Val Lys
 340 345 350

Asn His Ala His Leu Gly Ala Phe Ser Phe Gly Glu Ser Asp Asp Gly
 355 360 365

Asp Lys Val Tyr Gln Gln Lys Gly Phe Asn Leu Glu Arg Leu Met Lys
 370 375 380

Ile Phe Thr Ser Leu Arg Asn
 385 390

<210> 10

<211> 316

<212> PRT

<213> Methanococcus jannaschii

<400> 10

Met Val Lys Leu Ser Gly Val Tyr Lys Gly Met Arg Lys Gly Tyr Gly
 1 5 10 15

Glu Thr Leu Ile Glu Leu Gly Lys Lys Tyr Glu Asn Leu Val Val Leu
 20 25 30

Asp Ala Asp Leu Ser Gly Ser Thr Gln Thr Ala Met Phe Ala Lys Glu
 35 40 45

Phe Pro Glu Arg Phe Phe Asn Ala Gly Val Ala Glu Gln Asn Met Ile
 50 55 60

Gly Met Ala Ala Gly Leu Ala Thr Thr Gly Lys Ile Val Phe Ala Ser
 65 70 75 80

Ser Phe Ser Met Phe Ala Ser Gly Arg Ala Trp Glu Ile Ile Arg Asn
 85 90 95

Leu Val Ala Tyr Pro Lys Leu Asn Val Lys Ile Val Ala Thr His Ala
 100 105 110

Gly Ile Thr Val Gly Glu Asp Gly Ala Ser His Gln Met Cys Glu Asp
 115 120 125

Ile Ala Ile Met Arg Ala Ile Pro Asn Met Val Val Ile Ala Pro Thr
 130 135 140

Asp Tyr Tyr His Thr Lys Asn Val Ile Arg Thr Ile Ala Glu Tyr Lys
 145 150 155 160

Gly Pro Val Tyr Val Arg Met Pro Arg Arg Asp Thr Glu Ile Ile Tyr
 165 170 175

Glu Asn Glu Glu Glu Ala Thr Phe Glu Ile Gly Lys Gly Lys Ile Leu
 180 185 190
 Val Asp Gly Glu Asp Leu Thr Ile Ile Ala Thr Gly Glu Glu Val Pro
 195 200 205
 Glu Ala Leu Arg Ala Gly Glu Ile Leu Lys Glu Asn Gly Ile Ser Ala
 210 215 220
 Glu Ile Val Glu Met Ala Thr Ile Lys Pro Ile Asp Glu Glu Ile Ile
 225 230 235 240
 Lys Lys Ser Lys Asp Phe Val Val Thr Val Glu Asp His Ser Ile Ile
 245 250 255
 Gly Gly Leu Gly Gly Ala Val Ala Glu Val Ile Ala Ser Asn Gly Leu
 260 265 270
 Asn Lys Lys Leu Leu Arg Ile Gly Ile Asn Asp Val Phe Gly Arg Ser
 275 280 285
 Gly Lys Ala Asp Glu Leu Leu Lys Tyr Tyr Gly Leu Asp Gly Glu Ser
 290 295 300
 Ile Ala Lys Arg Ile Met Glu Glu Met Lys Lys Glu
 305 310 315

<210> 11
 <211> 409
 <212> PRT
 <213> *Bacillus thiaminolyticus*

<400> 11
 Met Ser Lys Val Lys Gly Phe Ile Tyr Lys Pro Leu Met Val Met Leu
 1 5 10 15
 Ala Leu Leu Leu Val Val Val Ser Pro Ala Gly Ala Gly Ala Ala His
 20 25 30
 Ser Asp Ala Ser Ser Asp Ile Thr Leu Lys Val Ala Ile Tyr Pro Tyr
 35 40 45
 Val Pro Asp Pro Ala Arg Phe Gln Ala Ala Val Leu Asp Gln Trp Gln
 50 55 60
 Arg Gln Glu Pro Gly Val Lys Leu Glu Phe Thr Asp Trp Asp Ser Tyr
 65 70 75 80
 Ser Ala Asp Pro Pro Asp Asp Leu Asp Val Phe Val Leu Asp Ser Ile
 85 90 95
 Phe Leu Ser His Phe Val Asp Ala Gly Tyr Leu Leu Pro Phe Gly Ser
 100 105 110
 Gln Asp Ile Asp Gln Ala Glu Asp Val Leu Pro Phe Ala Leu Gln Gly
 115 120 125

Ala Lys Arg Asn Gly Glu Val Tyr Gly Leu Pro Gln Ile Leu Cys Thr
 130 135 140

Asn Leu Leu Phe Tyr Arg Lys Gly Asp Leu Lys Ile Gly Gln Val Asp
 145 150 155 160

Asn Ile Tyr Glu Leu Tyr Lys Lys Ile Gly Thr Ser His Ser Glu Gln
 165 170 175

Ile Pro Pro Pro Gln Asn Lys Gly Leu Leu Ile Asn Met Ala Gly Gly
 180 185 190

Thr Thr Lys Ala Ser Met Tyr Leu Glu Ala Leu Ile Asp Val Thr Gly
 195 200 205

Gln Tyr Thr Glu Tyr Asp Leu Leu Pro Pro Leu Asp Pro Leu Asn Asp
 210 215 220

Lys Val Ile Arg Gly Leu Arg Leu Leu Ile Asn Met Ala Gly Glu Lys
 225 230 235 240

Pro Ser Gln Tyr Val Pro Glu Asp Gly Asp Ala Tyr Val Arg Ala Ser
 245 250 255

Trp Phe Ala Gln Gly Ser Gly Arg Ala Phe Ile Gly Tyr Ser Glu Ser
 260 265 270

Met Met Arg Met Gly Asp Tyr Ala Glu Gln Val Arg Phe Lys Pro Ile
 275 280 285

Ser Ser Ser Ala Gly Gln Asp Ile Pro Leu Phe Tyr Ser Asp Val Val
 290 295 300

Ser Val Asn Ser Lys Thr Ala His Pro Glu Leu Ala Lys Lys Leu Ala
 305 310 315 320

Asn Val Met Ala Ser Ala Asp Thr Val Glu Gln Ala Leu Arg Pro Gln
 325 330 335

Ala Asp Gly Gln Tyr Pro Gln Tyr Leu Leu Pro Ala Arg His Gln Val
 340 345 350

Tyr Glu Ala Leu Met Gln Asp Tyr Pro Ile Tyr Ser Glu Leu Ala Gln
 355 360 365

Ile Val Asn Lys Pro Ser Asn Arg Val Phe Arg Leu Gly Pro Glu Val
 370 375 380

Arg Thr Trp Leu Lys Asp Ala Lys Gln Val Leu Pro Glu Ala Leu Gly
 385 390 395 400

Leu Thr Asp Val Ser Ser Leu Ala Ser
 405

<210> 12
 <211> 13

<212> PRT
<213> Naegleria gruberi

<400> 12
Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
1 5 10

<210> 13
<211> 12
<212> PRT
<213> Naegleria gruberi

<400> 13
Thr Ile Leu Asp Ser Thr Val Val Ala Ser Gln Arg
1 5 10

<210> 14
<211> 15
<212> PRT
<213> Naegleria gruberi

<400> 14
Ser Ser Asn Phe Tyr Ala Gln Leu Ser Gln Gln Phe Asp Ala Lys
1 5 10 15

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
Cys Ala Arg Trp Ser Ile Gly Gly His Gly Ala Tyr Cys Ala Arg Gly
1 5 10 15

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
Thr Thr Ile Gly Cys Arg Thr Cys Arg Ala Ala Tyr Thr Gly Tyr Thr
1 5 10 15
Gly

<210> 17
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
tgtcggatat agtggaaagta'tg

22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
aacctttgc ttttcatcac ac

22

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
gagatataca tatgtccact caaccaaaga c

31

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
tatggatcct taaaggaatg gtctcaagac acc

33

<210> 21
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
caataaaaaag tttgagctca agtattg

27

<210> 22
<211> 13
<212> PRT
<213> *Naegleria gruberi*

<400> 22
Val Tyr Gly Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu
1 5 10

<210> 23
<211> 6
<212> PRT
<213> *Naegleria gruberi*

<400> 23
Gly Tyr Ser Glu Ser Met
1 5